

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 1, 2001, 15:47:10 ; Search time 210.42 Seconds  
(without alignments)  
101.564 Million cell updates/sec

Title: US-09-331-631A-5

Perfect score: 3326  
Sequence: 1 OCMOLETSGQMRVCVSCCDK.....SPRSRKQOQPLVSIIDPVGCF 625

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_36.\*  
1: /SIDSI/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SIDSI/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SIDSI/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SIDSI/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SIDSI/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SIDSI/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SIDSI/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SIDSI/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SIDSI/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SIDSI/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SIDSI/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SIDSI/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SIDSI/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SIDSI/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SIDSI/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SIDSI/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SIDSI/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SIDSI/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3326	100.0	625	19 W62830	Macadamia integrif
2	3227	97.0	666	19 W62828	Macadamia integrif
3	3215	96.7	666	19 W62829	Macadamia integrif
4	1116	33.6	566	13 R20181	Sequence encoded b
5	1092.5	32.8	590	19 W62832	Gossypium hirsutum
6	1015	30.5	525	19 W62831	Theobroma cacao an
7	888	26.7	593	19 W62835	Zea mays antimicro
8	864.5	26.0	637	19 W62837	Hordeum vulgare an
9	863.5	26.0	626	20 Y15244	Peanut allergen A
10	863.5	26.0	626	20 Y25657	Peanut allergen A
11	861	25.9	614	18 W22149	Peanut allergen Ar
12	861	25.9	614	19 W62834	Arachis hypogaea a

13	859.5	25.8	605	19 W62838
14	857.5	25.8	626	18 W22150
15	842.5	25.3	605	20 Y40999
16	794	23.9	524	20 W90339
17	776.5	23.3	489	20 W90341
18	743	22.3	444	20 W90340
19	724.5	21.8	415	20 Y40913
20	677.5	20.4	409	20 W90342
21	526.5	15.8	371	20 Y40914
22	216	6.5	1898	20 Y30795
23	199.5	6.0	1162	21 Y58500
24	199	6.0	611	21 Y29039
25	189	5.7	472	15 R47127
26	186.5	5.6	499	9 P82755
27	185.5	5.6	562	16 R70491
28	177	5.3	510	20 Y15246
29	176	5.3	512	20 Y40912
30	174.5	5.2	1239	20 Y55931
31	169.5	5.1	515	15 W03627
32	169	5.1	360	17 R47128
33	169	5.1	412	17 W03626
34	165.5	5.0	1233	20 Y55954
35	164	4.9	1135	21 Y68784
36	163	4.9	493	13 R28944
37	161.5	4.9	316	13 R26941
38	161	4.8	1299	21 Y55933
39	158.5	4.8	1326	20 Y55933
40	148	4.4	281	21 Y91958
41	148	4.4	1041	20 W30613
42	146.5	4.4	1297	20 Y55932
43	143.5	4.3	1805	13 R27204
44	143.5	4.3	1805	15 R60126
45	142	4.3	968	20 Y55966

#### ALIGNMENTS

RESULT	ID	W62830	standard: Protein: 625 AA.
XX	AC	W62830:	
XX	DT	27-OCT-1998 (first entry)	
XX	DE	Macadamia integrifolia antimicrobial protein.	
XX	KW	antimicrobial protein; infestation; control.	
XX	OS	Macadamia integrifolia.	
XX	XX		
FT	Key	Location/Qualifiers	
FT	Peptide	1..28	
FT	Protein	/note="signal peptide"	
FT		29..666	
XX		/note="mature protein"	
PN	W09827805-A1.		
PD	02-JUL-1998.		
XX			
PF	22-DEC-1997:	97WO-AU00874.	
XX			
PR	20-DEC-1996:	96AU-0004275.	
XX			
PA	(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.		
XX			
PI	Bower NT, Goulter KC, Green JL, Mannens JM, Marcus JP:		
XX			
DR	WPI: 1998-377279/32.		
XX	N-PSDB: V42316.		

Glycine max anti  
Peanut allergen Ar  
Soybean beta-congl  
G. max SBP1 protei  
G. max SBP2 protei  
G. max truncated S  
Ara h 1 allergen p  
G. max truncated S  
Phaseolin A chain  
A human trichophy  
HHV8 ORF 73 protei  
T. gondii immunoge  
Modified oat globi  
Rice storage prote  
Leucocytocoon prot  
Peanut allergen, A  
Ara h 3 allergen s  
Human ZC1 protein.  
Oat globulin A2B. A  
Human follicle sti  
Human thyrotropin  
Mouse STE20-relate  
Amino acid sequenc  
P. falciparum LSA g  
P. falciparum LSA-R  
Protein regulating  
Human ZC3 protein.  
Human cytoskeleton  
Human CDC28-#3 RNA  
Human ZC2 protein.  
Rat nestlin. Ratu  
Full length human

PT Novel anti-microbial protein from e.g. *Macadamia integrifolia* -  
 PT useful for controlling microbial infestations of plants or mammals  
 XX  
 XX  
 PS Claim 1: Page 43-45; 96pp; English.  
 XX  
 CC The sequence is that of an antimicrobial protein which can  
 CC be used to control microbial infestations in plants and mammalian  
 CC animals.  
 XX  
 SO Sequence 625 AA:

Query Match 100.0%; Score 3326; DB 19; Length 625;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-296;  
 Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OCMQLETSQGMRCVCSQCKRFEEDIDMSKYDNOEDPOTECOCQCRRCQOESDPQOQY 60  
 DB 1 qcmqlstsgmtrcvsqcdrlfeedldwskydnqdpqlecqgcqrrcqgesdprqyqy 60  
 QY 61 CORCKEICEEEEEYNRQDPQOQYEQCQRCQRRTEPRHMOICQORCERYEKEKRQ 120  
 DB 61 cqrckelceeeeynrqdpqyqgcqkrcqrreterphmqicqgreeryeketrq 120  
 QY 121 QKRYEEOQRDEDEKYERKMGEGDNKRDPOQREYEDCRHCEQOEPRLQYQCRQCOQOR 180  
 DB 121 qkryeeqqrdeedekyeernkeednkrdpqreyedcrrrceqgeprlqyqgcrrceqqr 180  
 QY 181 QHCRGDDLMNPOGSGRVEEGEESKSDNPYFDEKSLSTRFTEEGHLSYLENFGRSK 240  
 DB 181 qhrgsgddlmnpqgsgryveegeeksdnpyfdekslstrfteeeghlsvlenfygrsk 240  
 QY 241 LRLALKNYRLVLLANPNAFVLPTHLADAILLVIGRGALKMIRHNRRESYNLECGDYI 300  
 DB 241 llralknryrlvllanpnafvlpthldadaillvigrgalkmihndresynlecgdyi 300  
 QY 301 RLPAGTTFFYLINDNNERLHIAKFLQITISTPGQYKEFFPAGGONPEPYLSTSKELLEAA 360  
 DB 301 rlpagttfyllindnnerlhiakfllqitlstpgykeffpagggnpepylstskelleaa 360  
 QY 361 LNTQTRLRGVLGOOREGVIIRASOQIRELTPRDESESRMWHIRGGSERGPNYLFNKR 420  
 DB 361 lntqtrlrgvlgooREGVIIRASOQIRELTPRDESESRMWHIRGGSERGPNYLFNKR 420  
 QY 421 PLYSNKYGQAYEVKPEDYROLQDMDVSVFIANTQCSMMGPFFNTSTKVVVAASGEADV 480  
 DB 421 plynkyygqayevkpedyrolqdmdivsvfiantqcsmmgpfntstkvvvaasgeadv 480  
 QY 481 EMACPHLSGRHGGRGGGRKHEEEVEVHYEOVARLSKREAIYVLAGHPVYVSSGNEML 540  
 DB 481 emacphlsgrhggrgggrkheeevhyevvarlskrealivvlaghpvyvssgneml 540  
 QY 541 LPAFGINAAONHNENFLAGRENVLOQIEPQAMELAFASKEVEELFNSODESTFPQCP 600  
 DB 541 lfafgineqnmhnenflagrenvloqiepqamelafaskeveelfnsodeslfpqcp 600  
 QY 601 QHQOQSPRSTKQOQPLVSLDPVGF 625  
 DB 601 qhqqsprstkgqplvsldpvgf 625

RESULT 2  
 W62828 W62828 standard; Protein: 666 AA.  
 AC W62828;  
 DT 27-OCT-1998 (first entry)  
 XX Macadamia integrifolia antimicrobial protein.  
 DE  
 XX  
 KM antimicrobial protein; infestation; control.  
 XX

OS Macadamia integrifolia.  
 XX  
 XX Key Location/Qualifiers  
 FT Peptide 1..28  
 FT Protein /note= "signal peptide"  
 FT Protein 29..666  
 FT Protein /note= "mature protein"  
 XX  
 PN W09827805-A1.  
 PN  
 PD 02-JUL-1998.  
 PD  
 PF 22-DEC-1997; 97WO-AU00874.  
 PF  
 PR 20-DEC-1996; 96AU-0004275.  
 PR  
 XX (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.  
 PA  
 PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;  
 PI  
 DR WPI: 1998-377279/32.  
 DR N-PSDB: V42310.  
 DR  
 XX  
 PT Novel anti-microbial protein from e.g. *Macadamia integrifolia* -  
 PT useful for controlling microbial infestations of plants or mammals  
 PS  
 PS Claim 1: Page 34-36; 96pp; English.  
 XX  
 CC The sequence is that of an antimicrobial protein which can  
 CC be used to control microbial infestations in plants and mammalian  
 CC animals.  
 XX  
 SO Sequence 666 AA:

Query Match 97.0%; Score 3227; DB 19; Length 666;  
 Best Local Similarity 96.6%; Pred. No. 1.7e-287;  
 Matches 604; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 OCMQLETSQGMRCVCSQCKRFEEDIDMSKYDNOEDPOTECOCQCRRCQOESDPQOQY 60  
 DB 42 qcmqlstsgmtrcvsqcdrlfeedldwskydnqdpqlecqgcqrrcqgesdprqyqy 101  
 QY 61 CORCKEICEEEEEYNRQDPQOQYEQCQRCQRRTEPRHMOICQORCERYEKEKRQ 120  
 DB 102 cqrckelceeeeynrqdpqyqgcqkrcqrreterphmqicqgreeryeketrq 161  
 QY 121 QKRYEEOQRDEDEKYERKMGEGDNKRDPOQREYEDCRHCEQOEPRLQYQCRQCOQOR 180  
 DB 162 qkryeeqqrdeedekyeernkeednkrdpqreyedcrrrceqgeprlqyqgcrrceqqr 221  
 QY 181 QHCRGDDLMNPOGSGRVEEGEESKSDNPYFDEKSLSTRFTEEGHLSYLENFGRSK 240  
 DB 222 qhrgsgddlmnpqgsgryveegeeksdnpyfdekslstrfteeeghlsvlenfygrsk 281  
 QY 241 LRLALKNYRLVLLANPNAFVLPTHLADAILLVIGRGALKMIRHNRRESYNLECGDYI 300  
 DB 282 llralknryrlvllanpnafvlpthldadaillvigrgalkmihndresynlecgdyi 341  
 QY 301 RLPAGTTFFYLINDNNERLHIAKFLQITISTPGQYKEFFPAGGONPEPYLSTSKELLEAA 360  
 DB 342 rlpagttfyllindnnerlhiakfllqitlstpgykeffpagggnpepylstskelleaa 401  
 QY 361 LNTQTRLRGVLGOOREGVIIRASOQIRELTPRDESESRMWHIRGGSERGPNYLFNKR 420  
 DB 402 lntqtrlrgvlgooREGVIIRASOQIRELTPRDESESRMWHIRGGSERGPNYLFNKR 461  
 QY 421 PLYSNKYGQAYEVKPEDYROLQDMDVSVFIANTQCSMMGPFFNTSTKVVVAASGEADV 480  
 DB 462 plynkyygqayevkpedyrolqdmdivsvfiantqcsmmgpfntstkvvvaasgeadv 521  
 QY 481 EMACPHLSGRHGGRGGGRKHEEEVEVHYEOVARLSKREAIYVLAGHPVYVSSGNEML 540  
 DB 521 emacphlsgrhggrgggrkheeevhyevvarlskrealivvlaghpvyvssgneml 540

DB	522	emacphlsgthrgyrggkthneeedthyegvarliskrealvllaqhvvfvssgne11	561			
Qy	541	LFAFGINAGNNHNFLAGREERNVLOQIEPAMELAPASRKEVEELFNSODESTFFPGPR	600			
Db	582	lfafglnagnnhnflagrerenvlqgilepamelaafaaprkeveestfnsqdstffpgpr	641			
Qy	601	QHQQSPRSTKQOQPLVSTILDFYGF	625			
Db	642	qhqqspstlkqgpplvsildfygf	666			
RESULT 3						
W62829	ID W62829 standard; Protein; 666 AA.					
XX	W62829;					
AC	XX					
XX	XX					
DT	27-OCT-1998 (first entry)					
XX	XX					
DE	Macadamia integrifolia antimicrobial protein.					
XX	XX					
KW	antimicrobial protein; infestation; control.					
XX	XX					
OS	Macadamia integrifolia.					
XX	XX					
FH	Key Location/Qualifiers					
FT	Peptide 1..28					
FT	Protein /note= "signal peptide"					
FT	/note= "mature protein"					
XX	XX					
PN	W09827805-A1.					
XX	XX					
PD	02-JUL-1998.					
XX	XX					
PF	22-DEC-1997; 97MO-AU00874.					
XX	XX					
PR	20-DEC-1996; 96AU-0004275.					
XX	XX					
PA	(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.					
XX	XX					
PI	Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;					
XX	XX					
DR	WPI. 1998-377279/32.					
DR	N-PSDB; VA2311.					
XX	XX					
PT	Novel anti-microbial protein from e.g. Macadamia integrifolia -					
PT	useful for controlling microbial infestations of plants or mammals					
XX	XX					
PS	Claim 1; Page 39-41; 96pp; English.					
XX	XX					
CC	The sequence is that of an antimicrobial protein which can					
CC	be used to control microbial infestations in plants and mammalian					
CC	animals.					
XX	XX					
SQ	Sequence 666 AA;					
Query Match 96.7%; Score 3215; DB 19; Length 666;						
Best Local Similarity 96.6%; Pred. No. 2,1e-286;						
Matches 604; Conservative 7; Mismatches 14; Indels 0; Gaps 0.						
Qy	1	OCMOLETSQMRRCYSOCCKRFEEDIDMSKXYDNEPDEPTEOCOCORCHQOESDPDOOQY	60			
Db	42	qcmqletsqmrtrcvsgckrtfeedidwskyndqddpgdcqqrtrqgesgprqgy	101			
Qy	61	CRCKKEICEEEEEEYRNDPPOOYEOCCRCORRETEPRHMOICQRCERYEKEKRKO	120			
Db	102	cgrckelceeeeynrqddpgqyqgcqrctetprhmqtcqrterryekexkrg	161			
Qy	121	OKRYEEOQREDEDEKYEENKESGDNKRDPQOREYEDCRHCEQDEPRLOYOCORCOEOQR	180			
Db	162	qkryeeqqrdeekyeenkeednkrdpqrqeyedcrrhceqdeprqyqgcqrcreqqr	221			

QY	181	QNRGGDLMPNRGSGSGRYEEBEKEQSDNPYPYFPDEBSLSTRFRFEECHISYLENFGRSK	240
Db	222	qngrygddlmpnrgsgsgrryeegeeksdnpypfderststrfteeghisvlenfygrsk	281
QY	241	LRRLAKNRYRLVLEENPNNAFVLPFTLLDADALLVLVIGRGALAKMTHRDNRESYNLECGDVI	300
Db	282	llrrlknryrlvleennpnaflvptllddadallvlvgrgalakmthdrnresynlecgdvi	341
QY	301	RIPACTFEYLLNRDNNERLHIAKLQTLSTPQYKKEFPFAGQGNPEPYLSTFSKELLLEAA	360
Db	342	ripactfeyllardnnerlhiaqltstpqykeffpaggqnpelystfskellleaa	401
QY	361	LMTQFERLRGLVGGQREGVITIRASQEQIRELTRDSDSRKHHIRGGESSRGPNLEFNKR	420
Db	402	lmtqferlrvgvlggqregvitisasqeqirreltrdsserrwhlirgessrpgpnlfnkr	461
QY	421	PLYSNKGQAYEVKREPDYRQLODDMVSFVFINITQGSMMGPFENTRSTKVVVVAASGEADV	480
Db	462	plysnkgygqayevkrpdyrqldmdvsvflantlqgsmmgpfiflucstkvvasgeadv	521
QY	481	EMACPRLSGRHGRCGCGKRHEEEDVEHYEVOYRARLSKRAIVVLACHPVVVFSSGNDMLT	540
Db	522	emacprlsgrhrgcrgcgrheeedvhyeqvkarlskraealvpygnprvfvssgndmlt	581
QY	541	LEAFGIMQNNHENTLAREKNVLOQIEPQAMELAFASRKEVDELFNSODESIFFPQPR	600
Db	582	lfafignqnhenllaqrenvlgqlepgamelafaprkeveelfnsodesiffrpqr	641
QY	601	OHQOQSPRSTKQOQOPLVSTLDFVGE	625
Db	642	qhqqgsstskqqpvlsvlldfvgf	666
RESULT	4		
ID	R20181		
XX	R20181	standard: protein; 566 AA.	
AC	R20181:		
XX	DT	16-APR-1992 (first entry)	
XX	DE	Sequence encoded by 67 kD T. cacao protein cDNA.	
XX	KW	Cocoa; flavour; vicilin; seed storage protein.	
XX	OS	Theobroma cacao.	
XX	PN	W09119801-A.	
XX	PD	26-DEC-1991.	
XX	PF	07-JUN-1991; 91WO-GB00914.	
XX	PR	11-JUN-1990; 90GB-0013016.	
XX	PA	(MRSC ) MARS UK LTD.	
XX	PI	Spencer ME, Hodge R, Deakin EA, Ashton S;	
XX	DR	WPI: 1992-024418/03.	
XX	PT	N-PSDB: Q20377.	
XX	PS	Recombinant cocoa proteins - are responsible for flavour in cocoa	
XX	CC	beans and produced in large quantities using yeast and bacterial	
XX	CC	expression vectors	
XX	CC	Claim 4; Fig 2; 59pp; English.	
XX	CC	The inventors claim a 67 kD and 31 kD T. cacao protein, and	
XX	CC	fragments, and encoding DNAs. The 47 kD and 31 kD proteins are	
XX	CC	derived from the 67 kD precursor. T. cacao protein cDNA was	
XX	CC	detected in a cDNA library prepared from immature cocoa beans RNA	















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Db 351 eeInkvlfsreeggqgqrlqesviveIskeqIalSkraKssrkL-----ssedkpf 406
QY 415 nFNKRPLXSNKYGOAYEKRPEDYRLODMOVSVFIANTOGSMKGFNTRSTKVVVA 474
   ||::||::|||::||::|||::||::|||::||::|||::||::|||::||::|||::||:
Db 407 nlrstrdplysnklygfefelrpeknplrdldflsvdmegalllphnsraivliVn 466
QY 475 SGEADVENACPHLSGRHGGRGGRKHEEEVHYEO-----VRARLSKREALIVLAGHP 528
   ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::||:
Db 467 egdanlelv-----gIkeqqeqqeqqeqplevrykraeIsqgdlfvIpaYp 513
QY 529 VVFFVSSGNLILFAFGINAONNHENFLAGREBNVLAQIEPAMELAFASRKEVEELFN 588
   ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::||:
Db 514 vvv--natslnffaiqlnaenngrnflaagsqdnvIsqIpsvqelafpsaqavekIlk 571
QY 589 SODESIFFPGRHOQOQSFRSTKQOQPLVSL 620
   ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::||:
Db 572 ngresyfvdaqppkkkegnkgrk--gplssll 601

RESULT 14
W22150
ID W22150 standard; Protein: 626 AA.
XX
AC W22150;
DT 29-DEC-1997 (first entry)
XX
DE Peanut allergen Ara hI.
XX
KM Peanut; seed storage protein; allergen; allergy: hypersensitivity;
KM vaccine; anaphylactic shock; immunotherapy; therapy;
KM monoclonal antibody; ELISA; analysis; Ara hI.
OS
XX Arachis hypogaea strain Florunner.
XX
FH Key Location/Qualifiers
FT Peptide 1..22
FT Protein /label= Sig_peptide
FT /label= 23..626
FT /label= Mat_protein
FT Modified-site 521..523
FT /note= "N-glycosylation site"
FT
XX
PN W09724139-A1.
XX
PD 10-JUL-1997.
XX
PE 23-SEP-1996; 96MO-US15222.
XX
PR 04-MAR-1996; 96US-0610424.
PR 29-DEC-1995; 95US-0009455.
XX
PA (UYAR-) UNIV ARKANSAS.
XX
PI Bannan GA, Burks AW, Cockrell G, Helm RM, Stanley JS;
DR WPI: 1997-363453/33.
DR N-PSDB; T76613.
XX
PT Peanut allergens Ara hI and Ara hII - used for vaccination and in
PT two-site monoclonal antibody based ELISA
XX
PS Claim 31; Page 172; 354pp; English.
XX
CC This polypeptide comprises major peanut allergen Ara hI (W22149).
CC Its sequence was deduced from cDNA clone pAlb (T76613), isolated
CC from peanut seed cDNA using a primer (see T76616) based on an
CC isolated Ara hI peptide (see W24206). The sequence shows
CC significant homology with the vicilin family of seed storage
CC proteins of other legumes. The allergen is recognised by serum
CC IgE from a large proportion of individuals with peanut
CC hypersensitivity. Ara hI and Ara hII (see W24164) can be used to
CC raise monoclonal antibodies which are used in a specific two-site

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CC MAb ELISA for the detection of Ara hI or Ara hII (claimed). IgE-
CC binding Ara hI antigen epitopes (see W24165-87) may be used in
CC vaccines to protect against allergic reactions to peanut allergens,
CC e.g. anaphylactic shock.
SQ Sequence 626 AA:
Query Match 25.8%; Score 857.5; DB 18; Length 626;
Best Local Similarity 34.3%; Pred. No. 4,4e-70;
Matches 209; Conservative 113; Mismatches 209; Indels 79; Gaps 18;
QY 52 ESDPRQOQY---CORRKEICEEEEYVNRQDPQOQYEQRCRCRRETEPR-----H 101
   ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::||:
Db 26 kspylgktempcaqrcIqscqgepddlkqk-----acearckleYdprcvyprgh 78
QY 102 MGICQRCRRYKREKRNQOQRYEEOQRDEKYEERMEKQD--NKRDQOQYEDCRN 159
   ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::||:
Db 79 lqtlngfppg-ertgrgpdY-----ddrtprtreagrgwpgagpreteree--- 127
QY 160 CEQGEPLQYOCQRCQOEQO-----RQHGRCGLMNPORQSGRYEGEGEKQSDNPPYFDE 215
   ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::||:
Db 128 -dwrgpredw---trpslqgprkrtiregrege-----qewglpshvreetstnmpfyfs 179
QY 216 RSLSTRFTEEGHISVLENFYGRSKLLRALKNYRLVLEANDPAFLPTNIDADAILLVI 275
   ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::||:
Db 180 rtfstrgnggrfvlrqlfdrgrsfqnlqbnrlvqlaekprtlvl|pkhadadnl|vlq 239
QY 276 GGRGALKMHRNDRNSYNLECGDVRIRPAGITFYILNRNMRRLIAKFLQITSPGOYK 335
   ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::||:
Db 240 gqaelvtvaangnrksfnldeghalrtpsgflsyllnrhndqnlrvaklsmpvtqpgfte 299
QY 336 EFPFAGGQNPPEYLSFTFSKEILEALNMQTERLRGVL-----GQQR----- 376
   ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::||:
Db 300 dffpassrdqsyIqfstrnlleaafnaefneltvll|eenaggeeqgrttwsttse 359
QY 377 --EGVITRASQOIRELTRDSESRMRHIRGCESSRG---PYLFNKRPYLSNKGQA 430
   ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::||:
Db 360 nnegyIvkvskheveltkhaks-----vskkyseeegdltnpInlregepdlsmfghl 414
QY 431 YEVRPEQYR-QLQDMOVSVFIANTOGSMKGFNTRSTKVVVAVSGEADVENACPHLSG 489
   ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::||:
Db 415 fevkrpdknprqlqldlmmIltcvelkegalmpIphfnskanvIvvnkylgnlelvavrkeq 474
QY 490 RHGGRGGRKHE-EEEEVYEQVR---ARLSKREALIVLAGHPVVVSSGNLILFAFG 545
   ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::||:
Db 475 qgrgrreeedeedeegsnrevrrytarlkegdvflmpaahpvaInasselhll--gfg 532
QY 546 INAONNHENFLAGREBNVLAQIEPAMELAFASRKEVEELFNSODESIFFPGRHOQO 605
   ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::||:
Db 533 Inaennhriflagdkdnvldiekqakdiafpgsgeyveklknqkeshfvsarpgsqg 592
QY 606 SPRSTKQOQ 615
   ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::||:
Db 593 spspspeke 602

RESULT 15
Y40999
ID Y40999 standard; protein: 605 AA.
XX
AC Y40999;
DT 06-DEC-1999 (first entry)
XX
DE Soybean beta-conglycinin protein sequence.
XX
KM Peanut; allergen; Ara h I; IgE; immunoglobulin E; epitope; Ara h 3;
KM allergic reaction; soybean; beta-conglycinin.
OS Glycine max.
XX
PN W09945961-A1.

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